

OIEP

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/848,832

DATE: 05/16/2001
 TIME: 14:50:52

ENTERED

Input Set : A:\H0001-NP002 SEQLIST.TXT
 Output Set: N:\CRF3\05162001\I848832.raw

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4 <110> APPLICANT: Hooper, Douglas
5   Dietzschold, Bernhard
7 <120> TITLE OF INVENTION: RABIES VIRUS-SPECIFIC NEUTRALIZING HUMAN
8   MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
11 <130> FILE REFERENCE: H0001.NP0002
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/848,832
C--> 13 <141> CURRENT FILING DATE: 2001-05-04
13 <150> PRIOR APPLICATION NUMBER: 60/204,518
14 <151> PRIOR FILING DATE: 2000-05-16
16 <160> NUMBER OF SEQ ID NOS: 8
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1430
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapien
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27 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgagactc      120
28 tcctgtgcag cctctggatt cacctttagc aactatgcc a tgagctgggt ccgccaggct      180
29 ccagggaagg ggctggagtg ggtctcagct attagtgcta gtggtcatag cacatatttg      240
30 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      300
31 ctgcaaatga acagcctgag agccgaggac acggccgat attactgtgc gaaagatcga      360
32 gaggttacta tgatagtgt acttaatgga ggctttgact actggggcca ggaacccgg      420
33 gtcaccgtct cctccgcctc caccaagggc ccatcggtct tcccctggc accctcctcc      480
34 aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa      540
35 ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggtc      600
36 gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc      660
37 ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac      720
38 aagagagttg agcccaaate ttgtgacaaa actcacacat gccaccggtg cccagcacct      780
39 gaactcctgg ggggaccgtc agtcttctc ttcccccaa aacccaagga caccctcatg      840
40 atctccccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag      900
41 gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg      960
42 gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac      1020
43 tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc agcccccatc      1080
44 gagaaaacca tctccaaagc caaaggcgag ccccgagaac cacaggtgta caccctgccc      1140
45 ccatcccggg aggagatgac caagaaccag gtcagcctga cctgcctggt caaaggcttc      1200
46 tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag      1260
47 accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctatagcaa gtcaccgtg      1320
48 gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg      1380
49 cacaaccact acacgcagaa gagcctctcc ctgtccccgg gtaaatgagt      1430
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 708
53 <212> TYPE: DNA
54 <213> ORGANISM: Homo sapien
55 <400> SEQUENCE: 2
57 agcatggaag cccagctca gcttctcttc ctctgctac tctggctccc agataccacc      60
58 ggagaaattg tgttgacaca gtctccagcc accctgtctt tgtctccagg ggaaagagcc      120

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59 accctcgccct gcagggccag tcagactgct agcaggtact tagcctggta ccaacagaaa 180
60 cctggccagg ctcccagact cctcatctat gatacatcca acagggccac tggcatocca 240
61 gccaggttca gtggcagtgg gtctgggaca gacttcacto tctccatcag cagcctggag 300
62 cctgaagatt ttgcagttta ttactgtcag cagcgtttca actggccgtg gacgttcggc 360
63 caagggacca aggtggaatt caaacgaact gtggctgcac catctgtctt catcttccc 420
64 ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480
65 tatcccagag aggccaaagt acagtggaa gttggataacg ccctccaatc gggtaactcc 540
66 caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacccgt 600
67 acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 660
68 ggctgagct cgcccgtcac aaagagcttc aacaggggag agtggttag 708
70 <210> SEQ ID NO: 3
71 <211> LENGTH: 474
72 <212> TYPE: PRT
73 <213> ORGANISM: Homo sapien
75 <400> SEQUENCE: 3
76 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
77 1 5 10 15
78 Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
79 20 25 30
80 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
81 35 40 45
82 Ser Asn Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
83 50 55 60
84 Glu Trp Val Ser Ala Ile Ser Ala Ser Gly His Ser Thr Tyr Leu Ala
85 65 70 75 80
86 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
87 85 90 95
88 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
89 100 105 110
90 Tyr Tyr Cys Ala Lys Asp Arg Glu Val Thr Met Ile Val Val Leu Asn
91 115 120 125
92 Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Arg Val Thr Val Ser Ser
93 130 135 140
94 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
95 145 150 155 160
96 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
97 165 170 175
98 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
99 180 185 190
100 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
101 195 200 205
102 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
103 210 215 220
104 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
105 225 230 235 240
106 Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
107 245 250 255
108 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
109 260 265 270

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110 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
111           275           280           285
112 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
113       290           295           300
114 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
115 305           310           315           320
116 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
117           325           330           335
118 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
119       340           345           350
120 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
121       355           360           365
122 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
123       370           375           380
124 Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
125 385           390           395           400
126 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
127           405           410           415
128 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
129       420           425           430
130 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
131       435           440           445
132 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
133       450           455           460
134 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
135 465           470
137 <210> SEQ ID NO: 4
138 <211> LENGTH: 234
139 <212> TYPE: PRT
140 <213> ORGANISM: Homo sapien
142 <400> SEQUENCE: 4
143 Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
144 1           5           10           15
145 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
146       20           25           30
147 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ala Cys Arg Ala Ser Gln Thr
148       35           40           45
149 Ala Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
150       50           55           60
151 Arg Leu Leu Ile Tyr Asp Thr Ser Asn Arg Ala Thr Gly Ile Pro Ala
152 65           70           75           80
153 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser
154       85           90           95
155 Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Phe
156       100          105          110
157 Asn Trp Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Phe Lys Arg
158       115          120          125
159 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
160       130          135          140

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161 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
162 145                150                155                160
163 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
164                165                170                175
165 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
166                180                185                190
167 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
168                195                200                205
169 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
170 210                215                220
171 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
172 225                230
174 <210> SEQ ID NO: 5
175 <211> LENGTH: 20
176 <212> TYPE: DNA
177 <213> ORGANISM: Homo sapien
179 <400> SEQUENCE: 5
180 accatggagt ttgggctgag                                20
182 <210> SEQ ID NO: 6
183 <211> LENGTH: 20
184 <212> TYPE: DNA
185 <213> ORGANISM: Homo sapien
187 <400> SEQUENCE: 6
188 actcatttac ccggggacag                                20
190 <210> SEQ ID NO: 7
191 <211> LENGTH: 20
192 <212> TYPE: DNA
193 <213> ORGANISM: Homo sapien
195 <400> SEQUENCE: 7
196 agcatggaag ccccagctca                                20
198 <210> SEQ ID NO: 8
199 <211> LENGTH: 21
200 <212> TYPE: DNA
201 <213> ORGANISM: Homo sapien
203 <400> SEQUENCE: 8
204 ctotaacact ctcccctgtt g                                21

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date